



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
- (ii) TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/952235
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/460368
(B) FILING DATE: 02-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P0938P1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-5416
(B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids

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(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp	Ile	Met	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Thr	Val	Ser	Val	1	5	10	15
Gly	Glu	Lys	Val	Thr	Val	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu	20	25	30	
Tyr	Thr	Ser	Ser	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	35	40	45	
Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	50	55	60	
Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	65	70	75	
Asp	Phe	Thr	Leu	Thr	Ile	Thr	Ser	Val	Lys	Ala	Asp	Asp	Leu	Ala	80	85	90	
Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Ala	Tyr	Pro	Trp	Thr	Phe	Gly	95	100	105	
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	110	115	120	
Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	125	130	135	
Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	140	145	150	
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	155	160	165	
Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	170	175	180	
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	185	190	195	
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	200	205	210	

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 215 220

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glx	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Arg	Pro	Gly		1	5	10	15
Ala	Ser	Val	Lys	Met	Ser	Cys	Arg	Ala	Ser	Gly	Tyr	Thr	Phe	Thr		20	25	30	
Ser	Tyr	Trp	Leu	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu		35	40	45	
Glu	Trp	Ile	Gly	Met	Ile	Asp	Pro	Ser	Asn	Ser	Asp	Thr	Arg	Phe		50	55	60	
Asn	Pro	Asn	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Asn	Val	Asp	Arg	Ser		65	70	75	
Ser	Asn	Thr	Ala	Tyr	Met	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Ala	Asp		80	85	90	
Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Tyr	Gly	Ser	Tyr	Val	Ser	Pro		95	100	105	
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala		110	115	120	
Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys		125	130	135	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp		140	145	150	
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu		155	160	165	
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly		170	175	180	

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 185 190 195
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 200 205 210
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 215 220 225
 His Thr Ala Ala Pro
 230

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 660 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAC ATT ATG ATG TCC CAG TCT CCA TCC TCC CTA ACT 36
 Asp Ile Met Met Ser Gln Ser Pro Ser Ser Leu Thr
 1 5 10
 GTG TCA GTT GGA GAG AAG GTT ACT GTG AGC TGC AAG TCC 75
 Val Ser Val Gly Glu Lys Val Thr Val Ser Cys Lys Ser
 15 20 25
 AGT CAG TCC CTT TTA TAT ACT AGC AGT CAG AAG AAC TAC 114
 Ser Gln Ser Leu Leu Tyr Thr Ser Ser Gln Lys Asn Tyr
 30 35
 TTG GCC TGG TAC CAG CAG AAA CCA GGT CAG TCT CCT AAA 153
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
 40 45 50
 CTG CTG ATT TAC TGG GCA TCC ACT AGG GAA TCT GGG GTC 192
 Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 55 60
 CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC 231
 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75

ACT CTC ACC ATC ACC AGT GTG AAG GCT GAC GAC CTG GCA 270
 Thr Leu Thr Ile Thr Ser Val Lys Ala Asp Asp Leu Ala
 80 85 90

GTT TAT TAC TGT CAG CAA TAT TAT GCC TAT CCG TGG ACG 309
 Val Tyr Tyr Cys Gln Gln Tyr Tyr Ala Tyr Pro Trp Thr
 95 100

TTC GGT GGA GGC ACA AAG TTG GAG ATC AAA CGG ACC GTG 348
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 105 110 115

GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 387
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 120 125

CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG 426
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 130 135 140

AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG 465
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 145 150 155

GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT 504
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
 160 165

GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC 543
 Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 170 175 180

AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 582
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 185 190

CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG 621
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
 195 200 205

AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT 660
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215 220

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 690 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

SAG	GTT	CAG	CTG	CAG	CAG	TCT	GGG	CCT	GAA	CTG	GTG	36	
Glx	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val		
1				5					10				
AGG	CCT	GGG	GCT	TCA	GTG	AAA	ATG	TCC	TGC	AGG	GCT	TCG	75
Arg	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Arg	Ala	Ser	
		15				20					25		
GGC	TAT	ACC	TTC	ACC	AGC	TAC	TGG	TTG	CAC	TGG	GTT	AAA	114
Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Leu	His	Trp	Val	Lys	
			30						35				
CAG	AGG	CCT	GGA	CAA	GGC	CTT	GAG	TGG	ATT	GGC	ATG	ATT	153
Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Met	Ile	
	40					45					50		
GAT	CCT	TCC	AAT	AGT	GAC	ACT	AGG	TTT	AAT	CCG	AAC	TTC	192
Asp	Pro	Ser	Asn	Ser	Asp	Thr	Arg	Phe	Asn	Pro	Asn	Phe	
			55					60					
AAG	GAC	AAG	GCC	ACA	TTG	AAT	GTA	GAC	AGA	TCT	TCC	AAC	231
Lys	Asp	Lys	Ala	Thr	Leu	Asn	Val	Asp	Arg	Ser	Ser	Asn	
	65				70					75			
ACA	GCC	TAC	ATG	CTG	CTC	AGC	AGC	CTG	ACA	TCT	GCT	GAC	270
Thr	Ala	Tyr	Met	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Ala	Asp	
		80					85					90	
TCT	GCA	GTC	TAT	TAC	TGT	GCC	ACA	TAT	GGT	AGC	TAC	GTT	309
Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Tyr	Gly	Ser	Tyr	Val	
			95						100				
TCC	CCT	CTG	GAC	TAC	TGG	GGT	CAA	GGA	ACC	TCA	GTC	ACC	348
Ser	Pro	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	
	105					110					115		
GTC	TCT	TCC	GCC	TCC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	CCC	387
Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	
			120					125					

